CLAIMS

1. A protein comprising:
a) 4-α-helix bundle motif formed from the α-helices of ROP (repressor of primer) and
b) a redox centre.

2 The protein of Claim 1 wherein the redox centre is a metal, preferably iron or copper, is an iron-sulphur centre, haem, FMN or FAD and is preferably haem.

3. The protein of Claim 1 or 2 wherein the redox centre is bound to the protein, preferably coordinated by one or more of histidine, leucine, methionine or cysteine residues and more preferably by 2 histidine residues.

4. The protein of Claim 1 or 2 wherein the redox centre is covalently bound to the protein.

5. The protein of Claim 1 which has a redox mid-point potential in the range -485 to +320mV.

6. The protein of Claim 1 which has α-helix regions each having 60%, preferably 70% and more preferably 80% similarity or identity with the α-helix regions of sequence ID Nos. 1 and 3.

7. The protein of claim 6, wherein said four α-helix regions are connected by loops.

8. The protein of claim 7, wherein the four α-helices are joined in the order 1-1'-2'-2.

9. The protein of Claim 1 which is formed by connecting two wild type ROP proteins to obtain the 4-helix bundle as one continuous polypeptide having 60%, preferably 70% and more preferably 80% similarity or identity with sequence ID No. 8.

10. The protein of claim 9, wherein the histidine residues corresponding to H76, H78, H107 and H109 in sequence ID No. 8 are removed.

11. The protein of claim 9 or 10, wherein histidine, leucine, methionine or cysteine residues are introduced one or both positions corresponding to 56 and 113 in sequence ID No. 8, preferably histidines are introduced at both positions 56 and 113.

12. The protein of any preceeding claim which has a haem redox centre co-ordinated to the 4-α-helix bundle motif via two histidine residues.

13. The protein of claim 12 which has a mid-point potential in the range -400mV to +300MV.

14. The protein of claim 12 which has the sequence as indicated by sequence ID No. 11.

15. The protein of any one of claims 1 to 14 which has a stability, measured as the unfolding free energy when denaturant is added to the protein, of $\Delta G_{obs}{}^{H_2O} \geq$ wherein $y \geq 3.0$ kcal/mol.

16. A method of producing the protein of any one of claims 1 to 15 comprising
   i) expressing all four α-helices as a single polypeptide chain;
   ii) engineering the required mutations to enable redox centre binding;
   iii) expressing and purifying,or producing the redox centre binding mutant;
   iv) Incubating the protein with an excess of the redox centre.

17. A nucleotide sequence which encodes the protein of any one of claims 1 to 15 or a fragment thereof.

18. A vector comprising the nucleotide sequence of claim 17.

19. Use of the protein of any of claims 1 to 15 in a sequence of electron carriers and preferably an electron transfer chain.

20. A method of passing electrons along a sequence of electron carriers, in which each electron carrier is reduced and then oxidised or vice versa by electron movement and the sequence of electron carriers includes the protein of any one of claims 1 to 15.

21. An apparatus comprising the protein of any one of claims 1 to 15 associated with an electrode.

22. An apparatus according to claim 21 wherein the protein is adsorbed onto an electrode.